

In the Claims:

Please cancel claims 1-34. Please add the following new claims 35-59.

35. (New) An isolated nucleic acid fragment comprising a sequence of at least about 20 nucleotides from a *Brassicaceae* delta-15 fatty acid desaturase gene having at least one mutation, wherein said at least one mutation is effective for increasing levels of oleic acid in *Brassicaceae* seeds and wherein said sequence includes said at least one mutation.

36. (New) The nucleic acid fragment of claim 35, wherein said sequence comprises a full-length coding sequence of said gene.

37. (New) The nucleic acid fragment of claim 35, wherein said mutant desaturase gene encodes a microsomal gene product.

38. (New) The nucleic acid fragment of claim 35, wherein said at least one mutation comprises a mutation in a region of said desaturase gene encoding a His-Xaa-Xaa-Xaa-His amino acid motif.

39. (New) The nucleic acid fragment of claim 38, wherein said at least one mutation comprises a non-conservative amino acid substitution in said region.

40. (New) The nucleic acid fragment of claim 39, wherein said motif comprises the sequence His-Asp-Cys-Gly-His.

41. (New) The nucleic acid fragment of claim 40, wherein said at least one mutation comprises the sequence His-Lys-Cys-Gly-His.

42. (New) The nucleic acid fragment of claim 35, wherein said mutant desaturase gene is from a *Brassica napus* plant.

43. (New) A *Brassicaceae* plant containing a sequence of at least 20 nucleotides from a delta-15 fatty acid desaturase gene having at least one mutation, said at least one mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif and wherein said mutation confers an altered fatty acid composition in seeds of said plant.

44. (New) The plant of claim 43, wherein said plant contains a full-length coding sequence of said mutant gene.

45. (New) The plant of claim 43, wherein said mutation confers a decreased level of α -linolenic acid in said seeds.

46. (New) The plant of claim 43, wherein said mutant desaturase gene encodes a microsomal gene product.

47. (New) The plant of claim 43, wherein said at least one mutation comprises a non-conservative amino acid substitution in said region.

48. (New) The plant of claim 47, wherein said motif comprises the sequence His-Asp-Cys-Gly-His.

49. (New) The plant of claim 48, wherein said at least one mutation comprises the sequence His-Lys-Cys-Gly-His.

50. (New) The plant of claim 43, wherein said mutant desaturase gene is from a *Brassica napus* plant.

51. (New) The plant of claim 43, wherein said plant is a *Brassica napus* plant.

52. (New) A *Brassicaceae* plant containing:

a) a sequence of at least 20 nucleotides from a delta-15 fatty acid desaturase gene having at least one mutation, said at least one delta-15 gene mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif;

b) a sequence of at least 20 nucleotides from a delta-12 fatty acid desaturase gene having at least one mutation, said at least one delta-12 gene mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif; and

c) said delta-15 gene mutation and said delta-12 gene mutation conferring an altered fatty acid composition in seeds of said plant.

53. (New) The plant of claim 52, wherein said mutant genes confer a decreased level of α -linolenic acid in said seeds.

54. (New) A vegetable oil extracted from seeds produced by the plant of claim 43.

55. (New) The oil of claim 54, wherein, following crushing of said seeds and extraction of said oil, said seeds said oil has from about 0.5% to about 10.0% α -linolenic acid based on total fatty acid composition.

56. (New) A vegetable oil extracted from seeds produced by the plant of claim 52.

57. (New) A vegetable oil extracted from seeds produced by the plant of claim 53.

58. (New) A method for producing a *Brassicaceae* plant line, comprising the steps of:

- a) inducing mutagenesis in cells of a starting variety of a *Brassicaceae* species;
- b) obtaining progeny plants from said cells;
- c) identifying at least one of said progeny plants that contains a delta-15 fatty acid desaturase gene having at least one mutation, said at least one mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif;
- d) producing said plant line from said at least one progeny plant by self-pollination for at least three additional generations.

59. (New) The method of claim 58, wherein said identifying step comprises a technique selected from the group consisting of: PCR, 3SR, and direct polynucleotide sequencing.